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Research Article

Sedum simingshanense (Crassulaceae), a new species from Zhejiang, East China

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Abstract

In this paper, *Sedum simingshanense* **sp. nov.** is described as a new species based on morphological and molecular analyses, and its taxonomic relationships are discussed. Morphological analysis indicates *S. simingshanense* should be classified in the genus *Sedum* sect. *Sedum* and is distinct from the related species *S. xunvense* and *S. formosanum* in the morphology of its solitary, light green and smooth stems, flattened leaves, larger, obovate and spurless sepals, yellow anthers, 22–30 ovules per carpel, oblique follicles, and its habitat on shaded slopes or rocks. Phylogenetic analysis of sequences of the nuclear ribosomal internal transcribed spacer (ITS) also demonstrates that *S. simingshanense* has a highest similarity of only 97.22% with any known species and *S. formosanum* is the closest extant relative of the new species.

Key words: ITS, morphological characters, new species, phylogenetic analysis, *Sedum simingshanense*

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Introduction

Sedum Linnaeus (1753: 430) is the largest genus in the family Crassulaceae with about 470 succulent herbaceous to (sub-)shrubby species (Thiede and Eggli 2007). Species within this genus are widely distributed in the Northern Hemisphere, and are most diverse in the Mediterranean region, Central America, the Himalayas, and East Asia (Stephenson 1994; Thiede and Eggli 2007). *Sedum* can be easily distinguished by its usually alternate leaves, sessile carpels slightly connate at the base, free, mostly yellow or white petals and stamens in two whorls (Thiede and Eggli 2007). However, molecular studies have revealed that *Sedum* is a highly polyphyletic group (Nikulin et al. 2016) which may be due to the high morphological plasticity and variability within the genus (Carrillo-Reyes et al. 2009). In China, 121 species were recorded in the Flora of China (Fu and Ohba 2001). During the past 20 years, about 18 *Sedum* species have been newly described from China (Huang et al. 2023).

During the preparation of the latest edition of the Flora of Zhejiang, a province in southeastern China, botanical expeditions were conducted in Zhejiang and

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its neighboring regions, resulting in the discovery of a previously unidentified *Sedum* species in June 2023. The species is morphologically similar to species grouping in *Sedum* sect. *Sedum*, which is characterized by carpels and follicles adaxially gibbous in the Flora of China (Fu and Ohba 2001). These plants grow on shaded slopes or rocks at an elevation of about 100–650 m in Siming Mountain, Zhejiang.

While these plants have a biennial life form, solitary, robust, light green and smooth fertile stems, flattened leaves, larger, obovate, basally spurless sepals, yellow anthers, 22–30 ovules per carpel, and oblique follicles, they were similar but obviously distinguished from *S. xunvense* (with an annual life form, purple-red and ribbed fertile stems, basally spurred sepals, reddish-brown anthers, and 8–13 ovules) and *S. formosanum* (with a perennial life form, clustered fertile stems, thick and succulent leaves, linear-lanceolate and basally spurred sepals, and erect follicles). In particular, the spurless sepals of these plants were the key differences from both *S. xunvense* and *S. formosanum* which both have spurred sepals.

Living plants were collected and cultivated in Zhejiang Museum of Natural History. After in-depth and careful studies of living materials, we were unable to assign it to any species described so far. The new species keys out as *S. formosanum* in the key in the Flora of China (Fu and Ohba 2001). In order to characterize this putatively new species, we examined its morphological features, and performed molecular phylogenetic analyses in order to reconstruct its relationships with morphologically related species, such as *S. xunvense* and *S. formosanum.* As a result, the different morphological characteristics and geographical distribution, and the separate phylogenetic position of the populations allow us to refer to them as a species new to science, named *Sedum simingshanense*.

Materials and methods

Field work and sampling

The specimens were collected in Siming Mountain Geopark (Yuyao county, Zhejiang province) (29°45'46"N, 121°02'02"E, elevation 653.2 m, 9 Jun 2023, Xu 2869), Lingnan Longshan (Shangyu county, Zhejiang province) (29°44'58"N, 121°00'39"E, elevation 472.9 m, 9 Jun 2023, Xu 2867) and Lingnan Fengshuping (Shangyu county) (29°47'25"N, 121°00'49"E, elevation 100.4 m, 9 Jun 2023, Xu 2868). Voucher specimens were deposited at the herbarium of Zhejiang Museum of Natural History (ZM0067398, ZM0067385, ZM0067399). Morphological characters of the new species were examined by digital camera (Nikon, Japan), and were further compared to those of the morphologically similar species in the genus *Sedum*, i.e. *S. xunvense* and *S. formosanum*, with morphological data based on Tang and Huang (1993), Ohba (2001), Fu and Ohba (2001), Choi et al. (2020), Chai et al. (2024) and our own measurements (Table 1).

DNA extraction and sequencing

DNA was isolated from freshly collected leaves of the newly discovered species found in Simingshan Geopark and Lingnan Longshan of Shangyu county using the Tiangen plant genomic DNA extraction kit (Tiangen Biotech, Beijing). ITS primers ITS-A (5'-GGAAGGAGAAGTCGTAACAAGG-3') and ITS-4

Table 1. Main differences between *S. simingshanense* sp. nov. and the morphologically similar *S. xunvense*, *S. formosanum* and *S. alfredii*.

Characters	*S. simingshanense*#	*S. xunvense*^	*S. formosanum**,$,@	*S. alfredi*~
Life form	biennial	Annual	perennial	perennial
Habitat	on shaded slopes or rocks	damp ravines, rocks and mossy thickets	rocky crevices along the sea coast	shady moist rocks on forested slopes
Fertile stems	solitary, robust, light green, smooth	solitary, slender, purple-red, ribbed	clustered, robust, green or slightly red, smooth	clustered, purple-red or slightly red, smooth
Leaf blades	flattened, spatulate	flattened, obovate to spatulate	thick and succulent, obovate to spatulate or suborbicular	flattened, obovate, spatulate or linear-cuneate
Leaf size (cm)	1.5–3 × 0.6–0.8	1.3–1.8 × 0.5–0.6	1–1.5 × 0.8–1.2	1.2–3 × 0.2–0.6
Sepals (mm)	obovate, 4–7 × 0.6–4, spurless, free	spatulate to obovate, 2–4 × 0.8–2.8, shortly spurred, free	linear-lanceolate, 2–3 mm long, spurred	linear-spatulate, 3–5 × 1–1.5 mm, spurred
Anther colour	yellow	reddish-brown	yellow	reddish-brown
Ovule number per carpel	22–30	8–13	20–30	(unknown)
Follicles	oblique	Oblique	erect	oblique
Seed shape & size (mm)	oval-ellipsoid, 0.48–0.55 × 0.28–0.30	ellipsoid, 0.6–0.7 × 0.25–0.3	narrowly ellipsoid, 0.4–0.6 × ca. 0.1	ca. 0.6 long

Based on Chai et al. (2024)^, Ohba (2001)*, Tang and Huang (1993)$, Choi et al. (2020)@, Fu and Ohba (2001)~ and this paper (measurements at ZM)#

(5'-TCCTCCGCTTATTGATATGC-3') amplifying ITS1, 5.8S rDNA and ITS2 regions were taken from Blattner (1999) and White et al. (1990). PCR program started with 5 min of initial denaturation at 94 °C, followed by 35 cycles of denaturation for 20 sec at 98 °C, annealing for 30 sec at 58 °C Tm for ITS, extension for 45 sec at 68 °C, and final extension for 7 min at 68 °C with KODFX DNA Polymerase (KFX-101, TOYOBO). The PCR products were analyzed using a 1.5% agarose TAE gel and subsequently sequenced by the Beijing Genomics Institute (Shenzhen, China). The newly generated sequences from this study were deposited in the National Center for Biotechnology Information (NCBI) (GenBank accessions: PP464048, PP464049, see Suppl. material 2).

Data analysis

To ascertain the phylogenetic position of the newly discovered species, DNA sequences of species in genus *Sedum*, as well as additional outgroup species were used. ITS sequences sourced from the NCBI website (Suppl. material 2) were obtained for the purpose of constructing a phylogenetic tree with Eastern Asian species in the *Acre* clade (Crassulaceae) (Nikulin et al. 2016; Messerschmid et al. 2020; Chai et al. 2024). A total of 76 sequences (including two of *S. simingshanense* and three outgroup species), were selected for subsequent analysis. SeqMan software (Burland 2000) was utilized for the assembly and editing of complementary strands, sequence was aligned with MAFFT v7.505 (Katoh and Standley 2013) using '--auto' strategy and normal alignment mode. Ambiguously aligned fragments were removed using Gblocks 0.91b (Talavera and Castresana 2007) with the following parameter settings: minimum number of sequences for a conserved/flank position (39/39), maximum number of contiguous non-conserved positions (8), minimum length of a block (10),

allowed gap positions (with half). ModelFinder v2.2.0 (Kalyaanamoorthy et al. 2017) was used to select the best-fit model using BIC criterion. Best-fit model according to BIC: SYM+I+G4. Maximum likelihood phylogenies were inferred using IQ-TREE v2.2.0 (Nguyen et al. 2015) under the SYM+I+G4 model for 5000 ultrafast (Minh et al. 2013) bootstraps, approximate Bayes test (Anisimova et al. 2011), as well as the Shimodaira–Hasegawa–like approximate likelihood-ratio test (Guindon et al. 2010).

Folding pattern of secondary structure of ITS rRNA: ITS1 and ITS2 region alignment was guided by primary and secondary structure conservation manually (Goertzen et al. 2003; Nikulin et al. 2016). The mfold webserver (Zuker 2003) was used with default conditions to elucidate the folding pattern of secondary structure elements in divergent sequences.

Results and discussion

Morphological analysis

After field observation, floral morphological characters of the new species were investigated and compared to those of the related species. The new species, named *S. simingshanense*, was found to be clearly different from the other related species (Fig. 1, Table 1). It is mainly distinguished from them by its solitary, light green and smooth stems, flattened leaves, larger, obovate and spurless sepals, yellow anthers, 22–30 ovules per carpel, oblique follicles, and its habitat on shaded slopes or rocks. The distinguishing characteristics of the new species and the three relatives in the *Acre* clade are listed in detail in Table 1.

Phylogenetic analysis

Our ITS phylogenetic tree presents a topology similar to that of Huang et al. (2023). In addition to the ITS sequences used in the phylogenetic analysis by Huang et al. (2023), 8 ITS sequences most similar to *S. simingshanense*, in descending order, in *S. arisanense* (LC229273), *S. actinocarpum* (LC229264), *S. morrisonense* var. *kwanwuense* (LC229293), *S. brachyrinchum* var. *brachyrinchum* (LC229274), *S. arisanense* (LC229272), *S. danjoense* (LC260127) and *S. xunvense* (PL010356, PL012036) were selected through BLAST searches in the NCBI database (Fig. 2). The phylogenetic analysis shows that the new species *S. simingshanense* is sister to a clade in the *Acre* Clade including *S. formosanum* and eight further *Sedum* taxa, well supported by high ultrafast bootstrap (UFBS) values, Bayesian posteriors (PP) values and SH approximate likelihood ratio test (SH-aLRT) values (93/1/98, Fig. 2) when using Maximum Likelihood method.

According to the predictions, the crassulacean ITS1 and ITS2 are characterized by presence of four helices and five single-stranded areas each (Nikulin et al. 2016). Suppl. material 1 illustrates the proposed base pairing in ITS1 and ITS2 of *S. simingshanense* and *S. formosanum*. Even though related in the phylogenetic tree, *S. simingshanense* and *S. formosanum* have four differences in secondary structures. In ITS1, *S. simingshanense* had an additional loop in Helix I and a side loop (2 nt) changed to an inner loop in Helix III. In ITS2, the two species differed in the structure of Helix I (different position of side and inner loops) and the structure (size) of the terminal loop (3 vs. 6 nt) of Helix II.

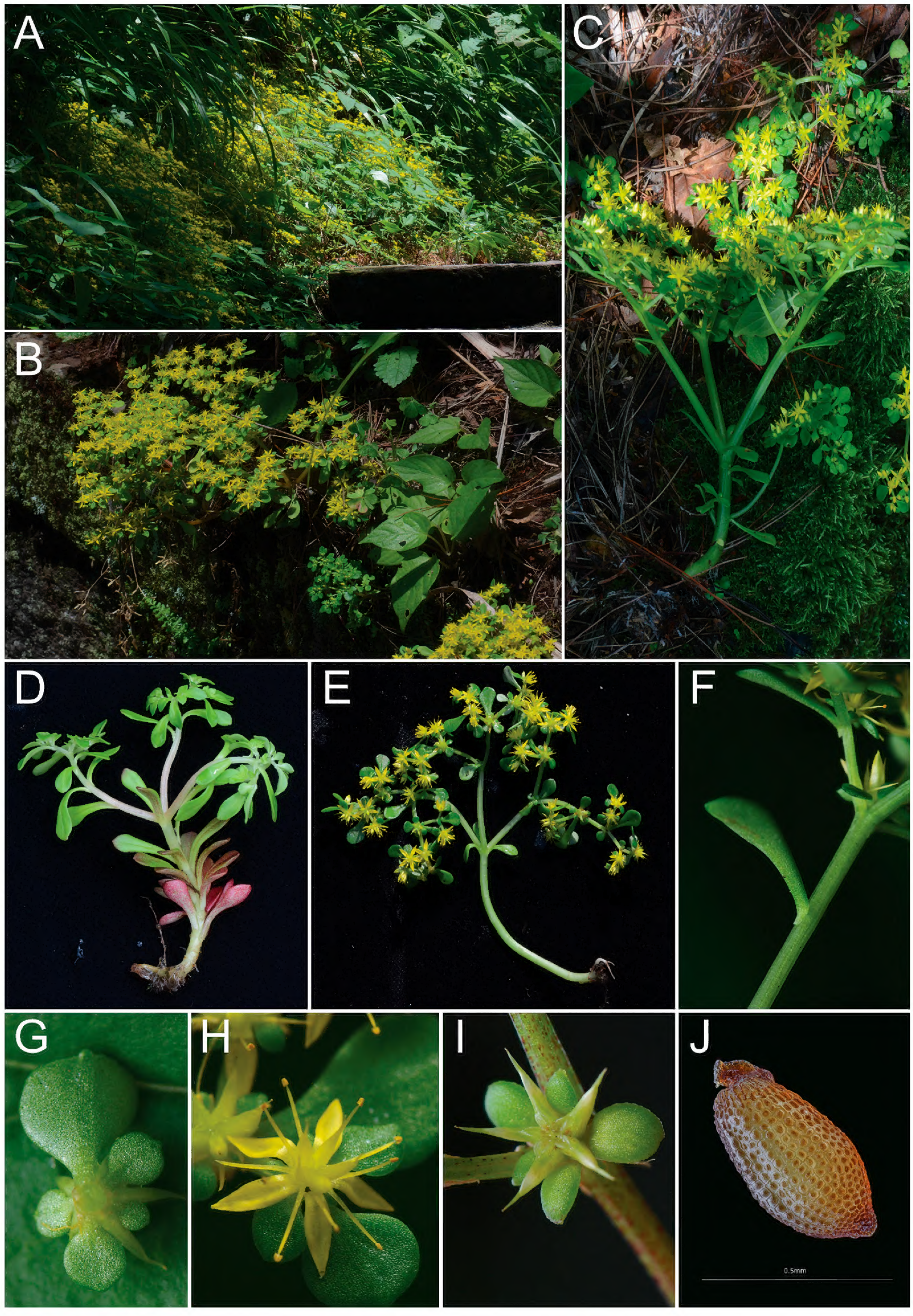

Figure 1. Morphology of *Sedum simingshanense* **A, B** natural habitat under shrubs in deciduous broad-leaved forests (from the type locality in Siming Mountain of Yuyao county, Zhejiang province) **C** flowering specimen **D** specimen before flowering **E** flowering specimen with immature follicles **F** leaf with basal spur **G** sepals from below **H** flower with sepals, petals, stamens and carpels **I** immature follicles **J** unripe seed **A–I** photographed by Yue-Liang Xu in the field (Siming Mountain Geopark, 9 Jun 2023, Xu 2869) **J** photographed by Jian-Sheng Wang in the lab (Lingnan Fengshuping, 9 Jun 2023, Xu 2868).

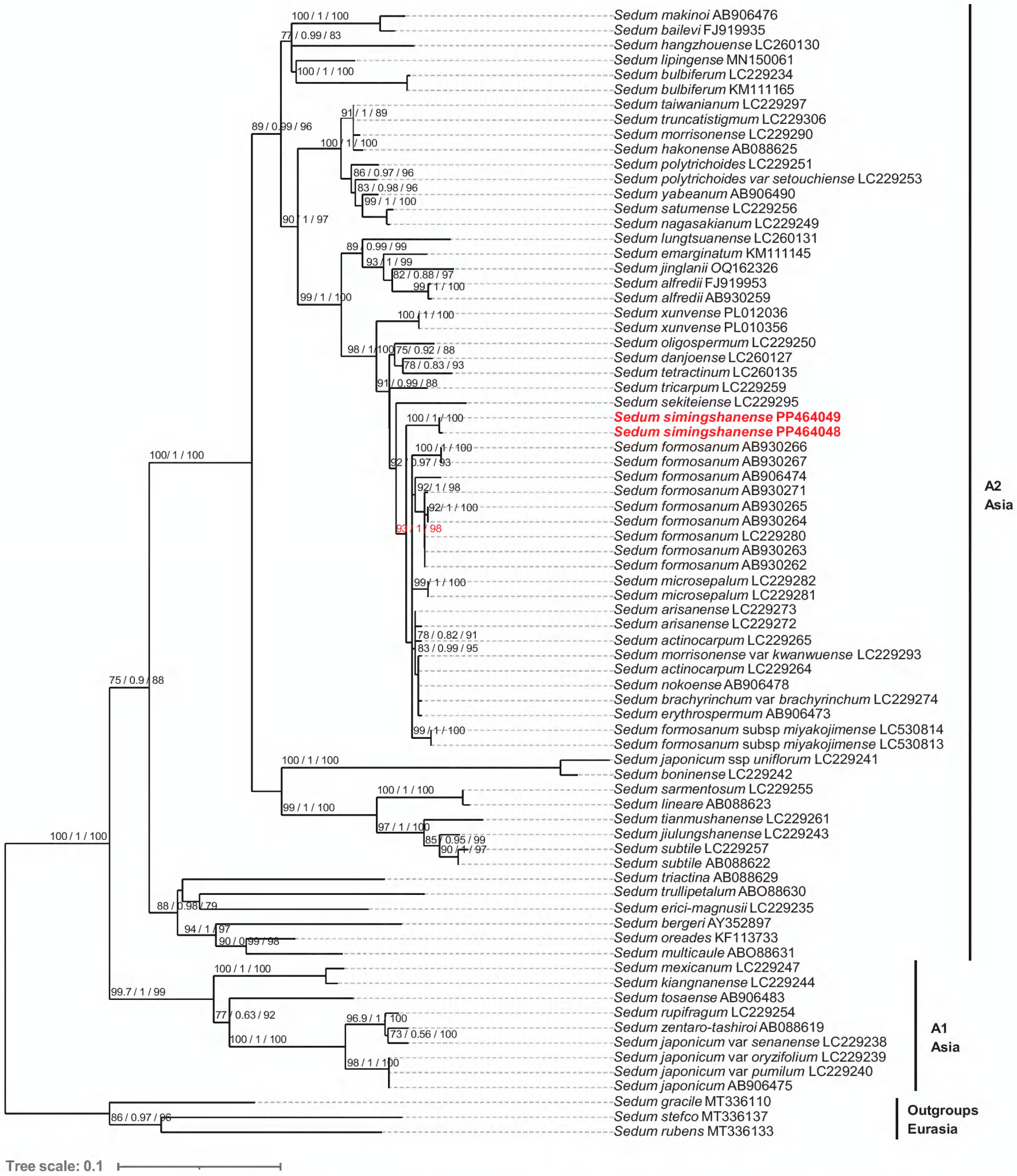

Figure 2. Maximum Likelihood tree based on ITS sequences for Eastern Asian species of the *Acre* clade, and three outgroups of the *Leucosedum* clade (Crassulaceae). Numbers near the branches are ultrafast bootstrap (UFBS) values, Bayesian posteriors (PP) values and SH approximate likelihood ratio test (SH-aLRT) values. UFBS values below 70 were ignored. The new species is highlighted in bold red. The accession numbers from Genbank are indicated after the scientific names. The two major clades in Asian *Sedum* are indicated with A1 and A2.

Discussion

The morphological analysis reveals that while *S. simingshanense*, *S. xunvense* and *S. formosanum* share some similar traits, they exhibit distinct characteristics. In addition to the general features of plants in *S. xunvense*, *S. simingshanense* plants were mainly characterized by its biennial life form (vs. an annual life form), the light green smooth stems (vs. slender, purple-red, ribbed),

sepals 4–7 × 0.6–4 mm, basally spurless (vs. 2–4 × 0.8–2.8 mm, basally shortly spurred), yellow anthers (vs. reddish brown), and 22–30 ovules per carpel (vs. 8–13). And in addition to the general features of plants in *S. formosanum*, *S. simingshanense* plants were mainly characterized by its biennial life form (vs. a perennial life form), being solitary (vs. clustered), stems green (vs. green or slightly red), leaves flattened (vs. thick and succulent), sepals obovate, 4–7 × 0.6–4 mm, basally spurless (vs. linear-lanceolate, 2–3 mm long, basally spurred), mature follicles obliquely ascending (vs. erect), and habitat on shaded slopes or rocks (vs. in rock crevices on seashore). In the key for sect. *Sedum* in the Flora of China (Fu and Ohba 2001), *S. simingshanense* keys out as *S. formosanum*, but differs from that species in its solitary stems while flowering stems of *S. formosanum* are branched from the base.

Furthermore, the molecular findings unambiguously indicate their separate phylogenetic positions. Together, the morphological and molecular evidence substantiate the conclusion that *S. simingshanense* is a distinct new species which groups in the *Acre* clade within the Crassulaceae and in sect. *Sedum* within the genus *Sedum*.

Sedum simingshanense has only been found in northeastern Zhejiang province of China, whereas *S. xunvense* has only been found in southwestern Zhejiang province (Chai et al. 2024; Fig. 4). *Sedum formosanum* is known to be distributed in the southern region of Japan, the northern islands of the Philippines, Hataedo Island and Sangtaedo Island of Korea, in Taiwan and Fujiang province of China (Rao 1996; Ito et al. 2014a; Choi et al. 2020; Ito et al. 2020). Highlighting the distinctions among these closely related species may provide insights into clarifying the taxonomic relationships within the *Acre* clade of *Sedum*.

Taxonomic treatment

***Sedum simingshanense* Y.L. Xu, sp. nov.**
urn:lsid:ipni.org:names:77354919-1
Figs 1, 3

Type. China • Zhejiang province, Yuyao county, Siming Mountains, Siming Mountain geopark, in roadside slope at forest edge, 29°45'46"N, 121°02'02"E, elevation 653.2 m, 9 Jun 2023, *Yue-Liang Xu*, *Xu 2869* (holotype: ZM barcode ZMNH0067398, Fig. 3).

Description. Biennial herbs, glabrous. Roots fibrous. No sterile stems when flowering. Fertile stems solitary, green, stout and succulent, smooth, branched from above the base into 3 branches, 10–20 cm tall, 5–8 mm in diam. Leaves alternate; leaf blade spatulate, flattened, 1.5–3 cm long, 0.6–0.8 cm wide, apex rounded, base gradually narrowed. Cymes many-flowered, first order branches 3-forked; bracts leaf-like, spatulate to obovate, 0.8–4 cm long, 0.4–1 cm wide, apex rounded, base attenuate into a 0.1–0.15 cm wide pseudopetiole, with short basal spur; flowers usually 5-parted, rarely 4-parted, sepals usually 5, rarely 4, unequal, obovate, thick and fleshy, 4–7 mm long, 0.6–4 mm wide, apex rounded or obtuse, base free, without spur; petals usually 5, rarely 4, yellow, lanceolate, 5–6 mm long, 1.3–2 mm wide, apex acute, base connate for ca. 0.5 mm; stamens usually 10, rarely 8, in 2 whorls, filaments filiform, those opposite to petals with filaments 3–4 mm long, fused with the base of the petal

Figure 3. Holotype of *Sedum simingshanense*. The specimen was collected in Siming Mountain Geopark (Yuyao county, Zhejiang province) (29°45'46"N, 121°02'02"E, elevation 653.2 m, 9 Jun 2023, Xu 2869) (ZMNH0067398).

for 1 mm, those opposite to sepals with filaments 4–5 mm long, completely free and not fused; anthers yellow; nectar scales usually 5, rarely 4, pale yellow, oblanceolate, ca. 0.5 mm long, ca. 0.25 mm wide; carpels usually 5, rarely 4, at anthesis upright, in unripe follicles spreading, ovate-lanceolate, 4.5–5 mm long, adaxially gibbous, basally connate for ca. 0.5 mm; styles ca. 0.8–1 mm; ovules 22–30 per carpel. Follicles obliquely diverging. Seeds light brown, oval-ellipsoid, 0.48–0.55 mm long, 0.28–0.30 mm in diam., densely minutely papillate.

Distribution and habitat. The new species is only known from Siming Mountains of Yuyao county, Zhejiang and Lingnan Longshan and Lingnan Fengshuping of Shangyu county, Zhejiang (Fig. 4). It grows on roadside slopes at the forest edge or on moss-covered stone walls at an elevation of about 100–650 m.

Phenology. Flowering from May to June, fruiting in June to July.

Etymology. The specific epithet '*simingshanense*' refers to the type locality of the new species.

Similar species. The new species is similar to *S. xunvense* and *S. formosanum*. It is mainly distinguished from them in the morphology of its solitary, light green and smooth stems, flattened leaves, larger, obovate and basally spurless sepals, yellow anthers, 22–30 ovules per carpel, oblique follicles, and its habitat on shaded slopes or rocks. In the vegetative state, it resembles *Sedum alfredii*, but S. *alfredii* has partly sterile and clustered stems, and purple-red or slightly red and smooth fertile stems (Fu and Ohba 2001). The distinguishing characteristics of the new species and the three morphological relatives are listed in detail in Table 1.

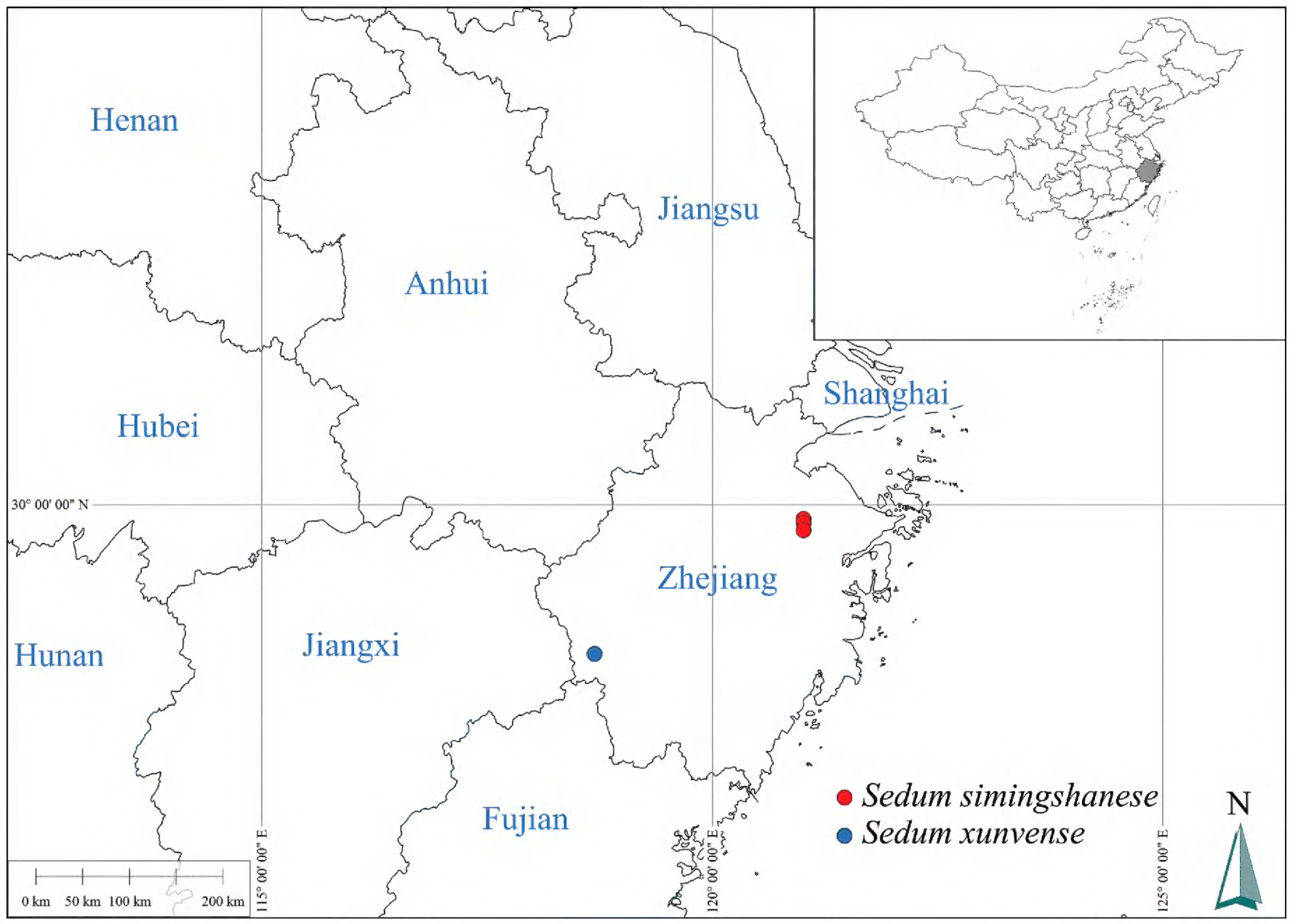

Figure 4. Geographical distribution of *Sedum simingshanense* (red dots) and *Sedum xunvense* (blue dots) in Zhejiang province of China. The insert map shows the situation of Zhejiang province within China.

Additional specimens examined (Paratypes). Lingnan Longshan, Shangyu county, roadside slope at forest edge, alt. 472.9 m, 29°44'58"N, 121°00'39"E, 9 Jun 2023, Yue-Liang Xu, Xu 2867 (ZM0067385); Lingnan Fengshuping, Shangyu county, on roadside rocks, alt. 100.4 m, 29°47'25"N, 121°00'49"E, 9 Jun 2023, Yue-Liang Xu, Xu 2868 (ZM0067399).

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

Conceptualization: YLX. Investigation: XXZ, SHY, YJP, YZ, XZ, SQS. Resources: YZ. Writing - original draft: SQS. Writing - review and editing: YLX, JY.

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Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

References

Anisimova M, Gil M, Dufayard JF, Dessimoz C, Gascuel O (2011) Survey of branch support methods demonstrates accuracy, power, and robustness of fast likelihood-based approximation schemes. Systematic Biology 60(5): 685–699. https://doi.org/10.1093/sysbio/syr041

Blattner FR (1999) Direct amplification of the entire ITS region from poorly preserved plant material using recombinant PCR. BioTechniques 27(6): 1180–1186. https://doi.org/10.2144/99276st04

Burland TG (2000) DNASTAR's Lasergene sequence analysis software. Methods in Molecular Biology (Clifton, N.J.) 132: 71–91. https://doi.org/10.1385/1-59259-192-2:71

Carrillo-Reyes P, Sosa V, Mort ME (2009) Molecular phylogeny of the Acre clade (Crassulaceae): Dealing with the lack of definitions for *Echeveria* and *Sedum*. Molecular Phylogenetics and Evolution 53(1): 267–276. https://doi.org/10.1016/j.ympev.2009.05.022

Chai M-L, Wu Y-M, Zhang Y, Pu J-B, Chen BIN, Xu Y-L, Li PAN (2024) *Sedum xunvense*, a new species from Southeast China. Phytotaxa 644(4): 258–270. https://doi.org/10.11646/phytotaxa.644.4.2

Choi SS, Kim J, Kim CH (2020) The taxonomic entity and distribution of Korean *Sedum formosanum* (Crassulaceae) revealed in 133 years. Korean Journal of Plant Taxonomy 50(4): 377–384. https://doi.org/10.11110/kjpt.2020.50.4.377

Fu KT, Ohba H (2001) Crassulaceae. In: Editorial Committee of Flora of China (Ed.) Flora of China 8. Missouri Botanical Garden Press, St. Louis, 202–268.

Goertzen LR, Cannone JJ, Gutell RR, Jansen RK (2003) ITS secondary structure derived from comparative analysis: Implications for sequence alignment and phylogeny of the Asteraceae. Molecular Phylogenetics and Evolution 29(2): 216–234. https://doi.org/10.1016/S1055-7903(03)00094-0

Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: Assessing the performance of PhyML 3.0. Systematic Biology 59(3): 307–321. https://doi.org/10.1093/sysbio/syq010

Huang YS, Meng KK, Sun YY, Chen ZX, Fan Q (2023) A new species of *Sedum* (Crassulaceae) from Mount Danxia in Guangdong, China. PhytoKeys 221: 117–129. https://doi.org/10.3897/phytokeys.221.97495

Ito T, Chen R, Yang Q-e, Saito Y, Yokota M, Kokubugata G (2014a) Taxonomic reexamination of *Sedum formosanum* (Crassulaceae) in Japan, Taiwan, and the Philippines based on molecular data. The Journal of Phytogeography and Taxonomy 62: 1–9. https://doi.org/10.24517/00053566

Ito T, Nakamura K, Park C, Song G, Maeda A, Watanabe Y, Kokubugata G (2014b) Nuclear and plastid DNA data confirm that *Sedum tosaense* (Crassulaceae) has a disjunct distribution between Pacific mainland Japan and Jeju Island, Korea. Phytotaxa 177(4): 221–230. https://doi.org/10.11646/phytotaxa.177.4.3

Ito T, Nakanishi H, Chichibu Y, Minoda K, Kokubugata G (2017a) *Sedum danjoense* (Crassulaceae), a new species of succulent plants from the Danjo Islands in Japan. Phytotaxa 309(1): 23–34. https://doi.org/10.11646/phytotaxa.309.1.2

Ito T, Yu CC, Nakamura K, Chung KF, Yang QE, Fu CX, Qi ZC, Kokubugata G (2017b) Unique parallel radiations of high-mountainous species of the genus *Sedum* (Crassulaceae) on the continental island of Taiwan. Molecular Phylogenetics and Evolution 113: 9–22. https://doi.org/10.1016/j.ympev.2017.03.028

Ito T, Yu CC, Yokota M, Kokubugata G (2020) *Sedum formosanum* subsp. *miyakojimense* (Crassulaceae), a new subspecies from Miyako-jima Island of the Ryukyu Islands, Japan. PhytoKeys 148: 51–70. https://doi.org/10.3897/phytokeys.148.48957

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. Nature Methods 14(6): 587–589. https://doi.org/10.1038/nmeth.4285

Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. Molecular Biology and Evolution 30(4): 772–780. https://doi.org/10.1093/molbev/mst010

Linnaeus C (1753) Species Plantarum. Tomus I. Imp. Laurentii Salvii, Holmiae, 560 pp.

Mayuzumi S, Ohba H (2004) The phylogenetic position of eastern Asian *Sedoideae* (Crassulaceae) inferred from chloroplast and nuclear DNA sequences. Systematic Botany 29(3): 587–598. https://doi.org/10.1600/0363644041744329

Messerschmid TFE, Klein JT, Kadereit G, Kadereit JW (2020) Linnaeus's folly – phylogeny, evolution and classification of *Sedum* (Crassulaceae) and Crassulaceae subfamily Sempervivoideae. Taxon 69(5): 892–926. https://doi.org/10.1002/tax.12316

Minh BQ, Nguyen MA, von Haeseler A (2013) Ultrafast approximation for phylogenetic bootstrap. Molecular Biology and Evolution 30(5): 1188–1195. https://doi.org/10.1093/molbev/mst024

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32(1): 268–274. https://doi.org/10.1093/molbev/msu300

Nikulin VY, Gontcharova SB, Stephenson R, Gontcharov AA (2016) Phylogenetic relationships between *Sedum* L. and related genera (Crassulaceae) based on ITS rDNA sequence comparisons. Flora (Jena) 224: 218–229. https://doi.org/10.1016/j.flora.2016.08.003

Ohba H (2001) Crassulaceae. In: Iwatsuki K, Boufford DE, Ohba H (Eds) Flora of Japan 2b. Kodansha, Tokyo, 21–29.

Rao GY (1996) Notes on Some Species of *Sedum* (Crassulaceae) in China. Journal of Systematics and Evolution 34: 621–626.

Stephenson R (1994) *Sedum*. Cultivated Stonecrops. Timber Press, 355 pp.

Talavera G, Castresana J (2007) Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. Systematic Biology 56(4): 564–577. https://doi.org/10.1080/10635150701472164

Tang WS, Huang TC (1993) Crassulaceae. In: Huang TC (Ed.) Flora of Taiwan. Department of Botany, National Taiwan University vol. 3, Taipei, 15–34.

Thiede J, Eggli U (2007) Crassulaceae. In: Kubitzki K (Ed.) The Families and Genera of Vascular Plants vol 9. Springer, Berlin Heidelberg, 83–118. https://doi.org/10.1007/978-3-540-32219-1_12

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and Direct Sequencing of Fungal Ribosomal RNA Genes for Phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR Protocols. Academic Press, San Diego, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Xie DM, Peng DY, Fang CW, Qin MJ, Wang DQ, Huang LQ (2014) *Sedum spiralifolium* (Crassulaceae): A new species from Anhui Province, China. Phytotaxa 183(3): 171–182. https://doi.org/10.11646/phytotaxa.183.3.4

Zhang JQ, Meng SY, Wen J, Rao GY (2014) Phylogenetic Relationships and Character Evolution of *Rhodiola* (Crassulaceae) based on Nuclear Ribosomal ITS and Plastid trnL-F and psbA-trnH Sequences. Systematic Botany 39(2): 441–451. https://doi.org/10.1600/036364414X680753

Zhang RB, Deng T, Dou QL, He L, Lv XY, Jiang H (2019) *Sedum lipingense* (Crassulaceae) identifying a new stonecrop species in SE Guizhou, China, based on morphological and molecular evidence. PhytoKeys 134: 125–133. https://doi.org/10.3897/phytokeys.134.38287

Zuker M (2003) Mfold web server for nucleic acid folding and hybridization prediction. Nucleic Acids Research 31(13): 3406–3415. https://doi.org/10.1093/nar/gkg595

Supplementary material 1

ITS1 and ITS2 secondary structure analysis of *Sedum simingshanense* and *Sedum formosanum* based on Mfold predictions

Authors: Shi-Qi She, Yang Zhang, Xin Zhou, Ya-Jun Peng, Shen-Hao Yao, Xing-Xing Zhao, Jia Yang, Yue-Liang Xu

Data type: tif

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Supplementary material 2

Origin, source and GenBank accession numbers of *Sedum* sequences and three outgroups used for phylogenetic analyses

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Data type: pdf

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